Figure 1A
Prostate Derived Ets Factor

```
   1  GTCTGACTTCCTCCCAGCACATTCCTGCACTCTGCCGTGTCCACACTGCCCCACAGACCC   60

  61  AGTCCTCCAAGCCTGCTGCCAGCTCCCTGCAAGCCCCTCAGGTTGGGCCTTGCCACGGTG  120

 121  CCAGCAGGCAGCCCTGGGCTGGGGGTAGGGGACTCCCTACAGGCACGCAGCCCTGAGACC  180

 181  TCAGAGGGCCACCCCTTGAGGGTGGCCAGGCCCCCAGTGGCCAACCTGAGTGCTGCCTCT  240

 241  GCCACCAGCCCTGCTGGCCCCTGGTTCCGCTGGCCCCCCAGATGCCTGGCTGAGACACGC  300

 301  CAGTGGCCTCAGCTGCCCACACCTCTTCCCGGCCCCTGAAGTTGGCACTGCAGCAGACAG  360

 361  CTCCCTGGGCACCAGGCAGCTAACAGACACAGCCGCCAGCCCAAACAGCAGCGGCATGGG  420
   1                                                      M  G    2

 421  CAGCGCCAGCCCGGGTCTGAGCAGCGTATCCCCCAGCCACCTCCTGCTGCCCCCCGACAC  480
   3   S  A  S  P  G  L  S  S  V  S  P  S  H  L  L  L  P  P  D  T   22

 481  GGTGTCGCGGACAGGCTTGGAGAAGGCGGCAGCGGGGGCAGTGGGTCTCGAGAGACGGGA  540
  23   V  S  R  T  G  L  E  K  A  A  A  G  A  V  G  L  E  R  R  D   42

 541  CTGGAGTCCCAGTCCACCCGCCACGCCCGAGCAGGGCCTGTCCGCCTTCTACCTCTCCTA  600
  43   W  S  P  S  P  P  A  T  P  E  Q  G  L  S  A  F  Y  L  S  Y   62

 601  CTTTGACATGCTGTACCCTGAGGACAGCAGCTGGGCAGCCAAGGCCCCTGGGGCCAGCAG  660
  63   F  D  M  L  Y  P  E  D  S  S  W  A  A  K  A  P  G  A  S  S   82

 661  TCGGGAGGAGCCACCTGAGGAGCCTGAGCAGTGCCCGGTCATTGACAGCCAAGCCCCAGC  720
  83   R  E  E  P  P  E  E  P  E  Q  C  P  V  I  D  S  Q  A  P  A  102

 721  GGGCAGCCTGGACTTGGTGCCCGGCGGGCTGACCTTGGAGGAGCACTCGCTGGAGCAGGT  780
 103   G  S  L  D  L  V  P  G  G  L  T  L  E  E  H  S  L  E  Q  V  122

 781  GCAGTCCATGGTGGTGGGCGAAGTGCTCAAGGACATCGAGACGGCCTGCAAGCTGCTCAA  840
 123   Q  S  M  V  V  G  E  V  L  K  D  I  E  T  A  C  K  L  L  N  142

 841  CATCACCGCAGATCCCATGGACTGGAGCCCCAGCAATGTGCAGAAGTGGCTCCTGTGGAC  900
 143   I  T  A  D  P  M  D  W  S  P  S  N  V  Q  K  W  L  L  W  T  162
```

Figure 1B
Prostate Derived Ets Factor

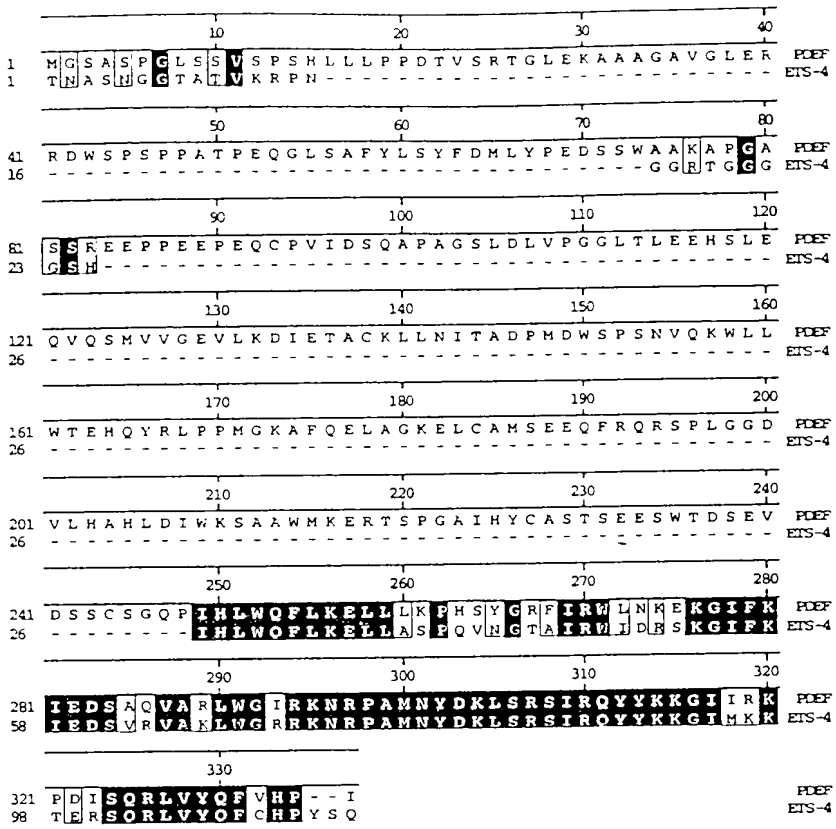
```
901  AGAGCACCAATACCGGCTGCCCCCCATGGGCAAGGCCTTCCAGGAGCTGGCGGGCAAGGA  960
163   E  H  Q  Y  R  L  P  P  M  G  K  A  F  Q  E  L  A  G  K  E   182

961  GCTGTGCGCCATGTCGGAGGAGCAGTTCCGCCAGCGCTCGCCCCTGGGTGGGGATGTGCT  1020
183   L  C  A  M  S  E  E  Q  F  R  Q  R  S  P  L  G  G  D  V  L   202

1021 GCACGCCCACCTGGACATCTGGAAGTCAGCGGCCTGGATGAAAGAGCGGACTTCACCTGG  1080
203   H  A  H  L  D  I  W  K  S  A  A  W  M  K  E  R  T  S  P  G   222

1081 GGCGATTCACTACTGTGCCTCGACCAGTGAGGAGAGCTGGACCGACAGCGAGGTGGACTC  1140
223   A  I  H  Y  C  A  S  T  S  E  E  S  W  T  D  S  E  V  D  S   242

1141 ATCATGCTCCGGGCAGCCCATCCACCTGTGGCAGTTCCTCAAGGAGTTGCTACTCAAGCC  1200
243   S  C  S  G  Q  P  I  H  L  W  Q  F  L  K  E  L  L  L  K  P   262

1201 CCACAGCTATGGCCGCTTCATTAGGTGGCTCAACAAGGAGAAGGGCATCTTCAAAATTGA  1260
263   H  S  Y  G  R  F  I  R  W  L  N  K  E  K  G  I  F  K  I  E   282

1261 GGACTCAGCCCAGGTGGCCCGGCTGTGGGGCATCCGCAAGAACCGTCCCGCCATGAACTA  1320
283   D  S  A  Q  V  A  R  L  W  G  I  R  K  N  R  P  A  M  N  Y   302

1321 CGACAAGCTGAGCCGCTCCATCCGCCAGTATTACAAGAAGGGCATCATCCGGAAGCCAGA  1380
303   D  K  L  S  R  S  I  R  Q  Y  Y  K  K  G  I  I  R  K  P  D   322

1381 CATCTCCCAGCGCCTCGTCTACCAGTTCGTGCACCCCATCTGAGTGCCTGGCCCAGGGCC  1440
323   I  S  Q  R  L  V  Y  Q  F  V  H  P  I  *                    336

1441 TGAAACCCGCCCTCAGGGGCCTCTCTCCTGCCTGCCCTGCCTCAGCCAGGCCCTGAGATG  1500

1501 GGGGAAAACGGGCAGTCTGCTCTGCTGCTCTGACCTTCCAGAGCCCAAGGTCAGGGAGGG  1560

1561 GCAACCAACTGCCCCAGGGGGATATGGGTCCTCTGGGGCCTTCGGGACCATGGGGCAGGG  1620

1621 GTGCTTCCTCCTCAGGCCCAGCTGCTCCCCTGGAGGACAGAGGGAGACAGGGCTGCTCCC  1680

1681 CAACACCTGCCTCTGACCCCAGCATTTCCAGAGCAGAGCCTACAGAAGGGCAGTGACTCG  1740

1741 ACAAAGGCCACAGGCAGTCCAGGCCTCTCTCTGCTCCATCCCCCTGCCTCCCATTCTGCA  1800
```

Figure 1C
Prostate Derived Ets Factor

1801 CCACACCTGGCATGGTGCAGGGAGACATCTGCACCCCTGAGTTGGGCAGCCAGGAGTGCC 1860

1861 CCCGGGAATGGATAATAAAGATACTAGAGAACTG 1894

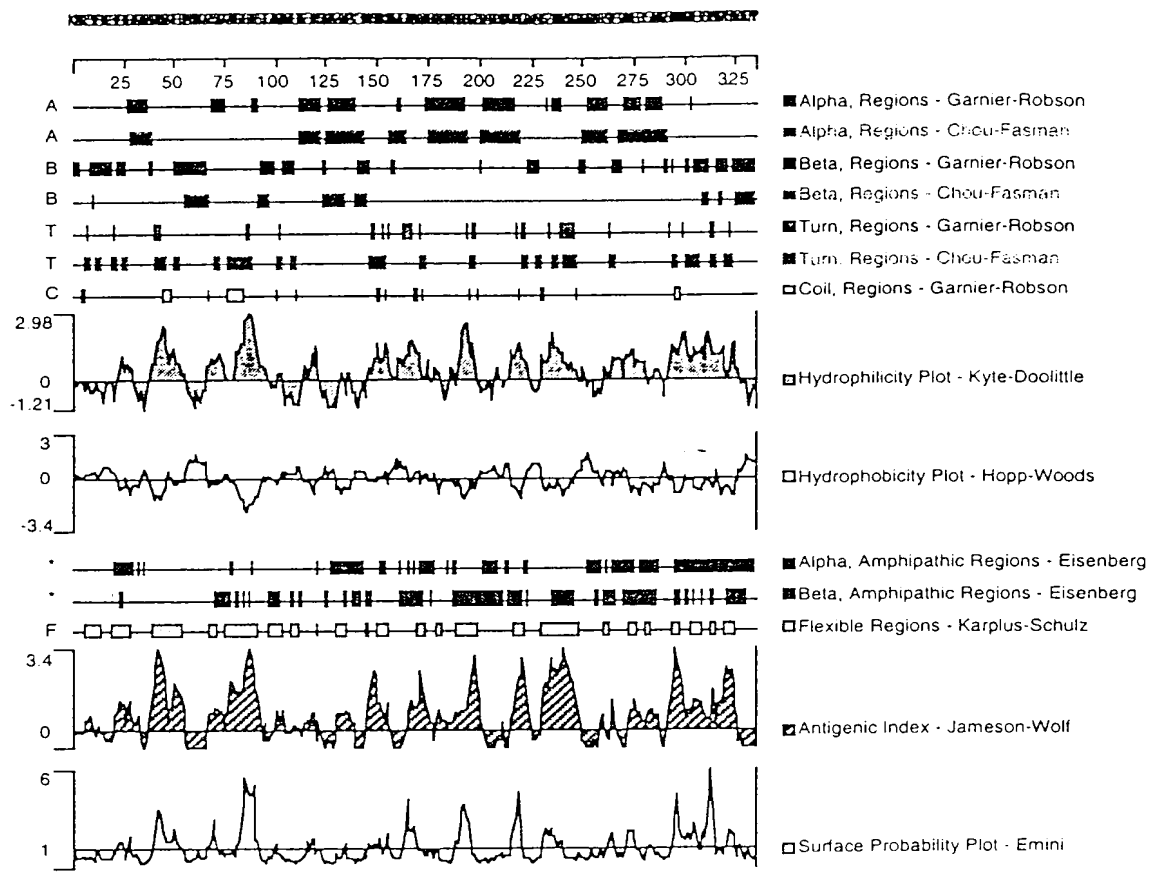
Figure 2



Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

Figure 3


25 50 75 100 125 150 175 200 225 250 275 300 325
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
2.98
0
-1.21
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini

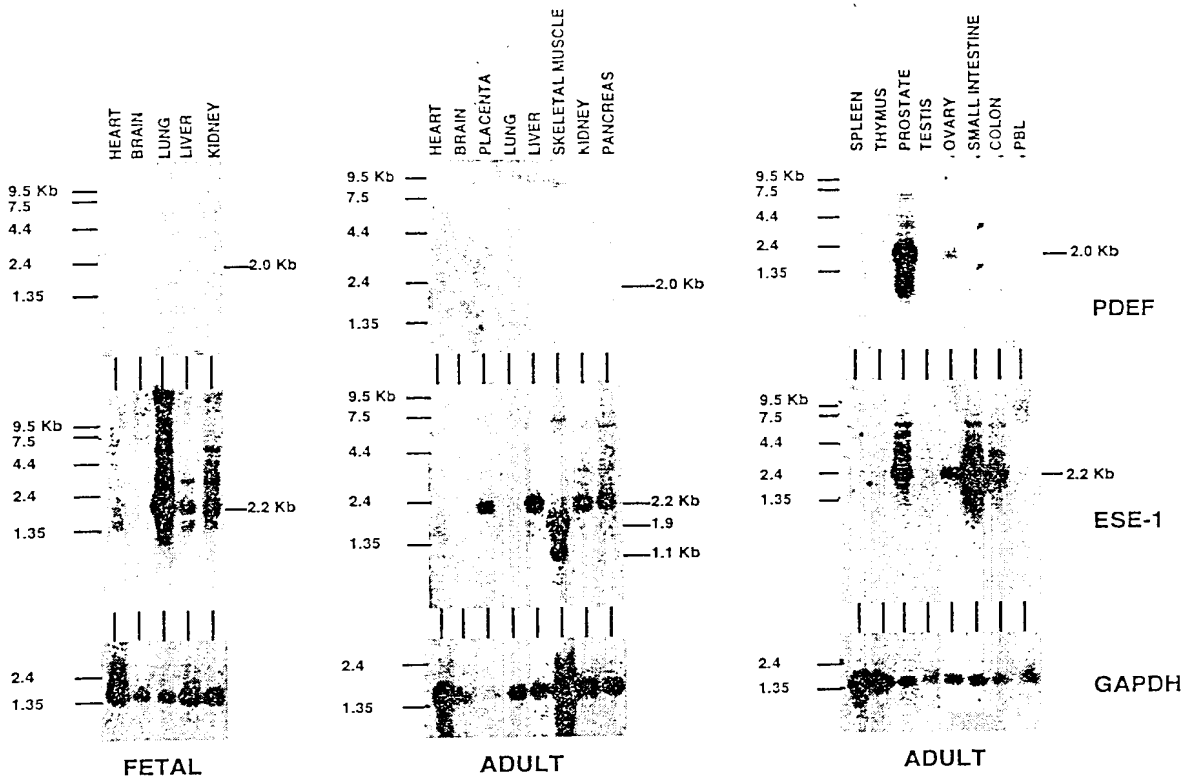
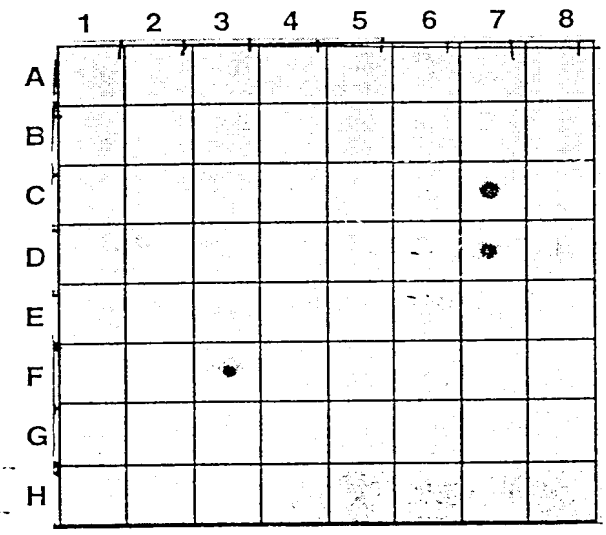


FIGURE 4



	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	subthalamic nucleus	spinal cord	
C	heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast RNA	yeast tRNA	E. coli rRNA	E. coli DNA	Poly r(A)	human C_0t1 DNA	human DNA 100 ng	human DNA 500 ng

FIGURE 5

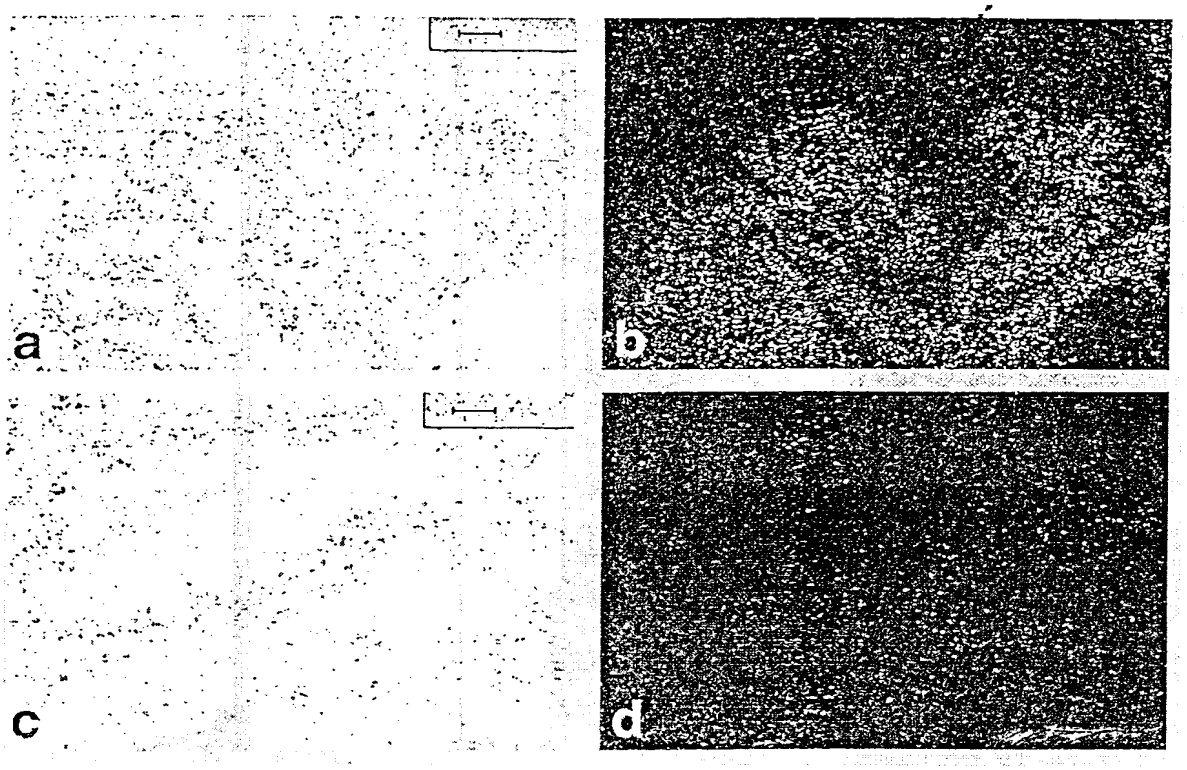


Figure 6

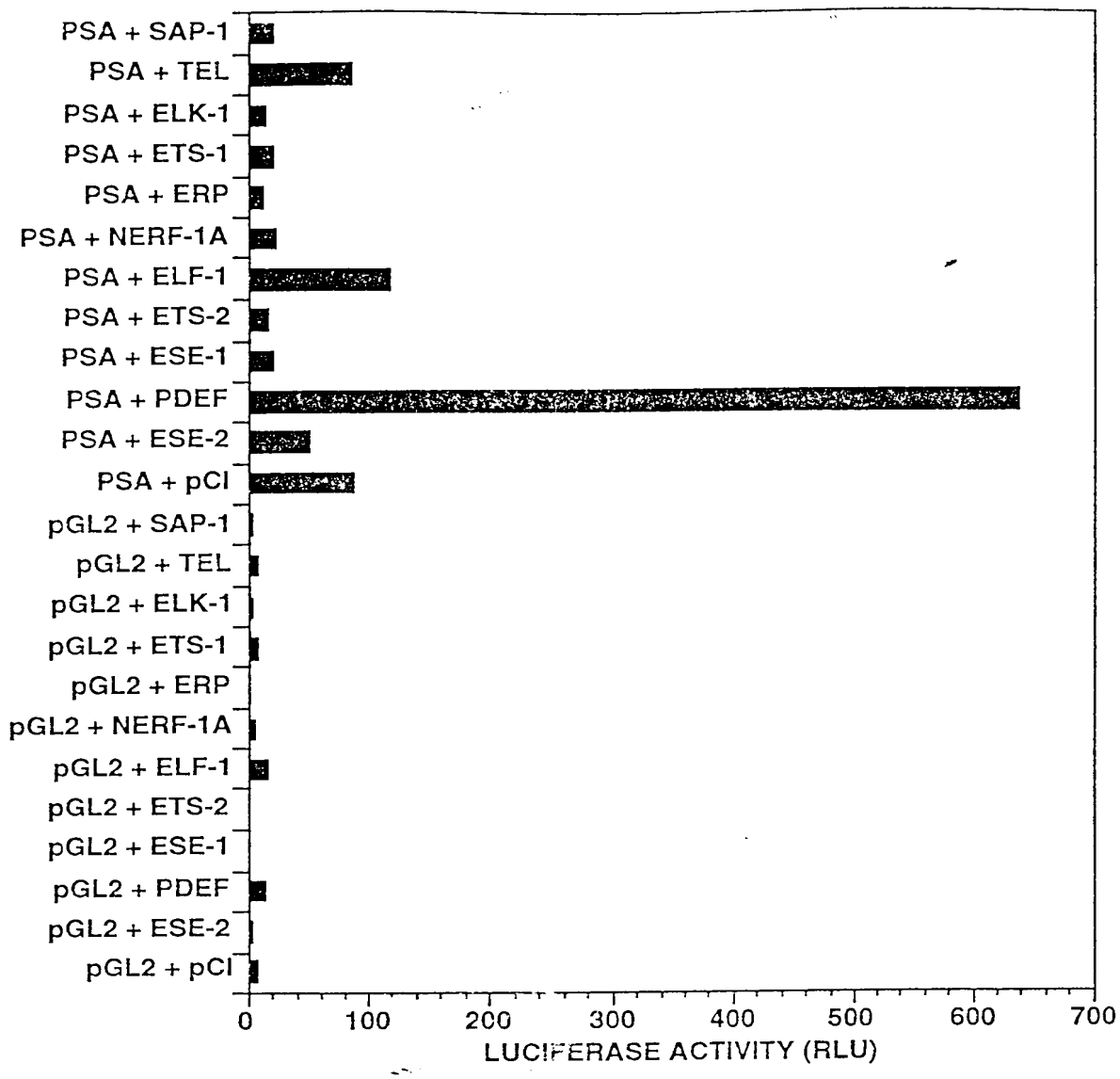

PSA + SAP-1
PSA + TEL
PSA + ELK-1
PSA + ETS-1
PSA + ERP
PSA + NERF-1A
PSA + ELF-1
PSA + ETS-2
PSA + ESE-1
PSA + PDEF
PSA + ESE-2
PSA + pCI
pGL2 + SAP-1
pGL2 + TEL
pGL2 + ELK-1
pGL2 + ETS-1
pGL2 + ERP
pGL2 + NERF-1A
pGL2 + ELF-1
pGL2 + ETS-2
pGL2 + ESE-1
pGL2 + PDEF
pGL2 + ESE-2
pGL2 + pCI
0
100
200
300
400
500
600
700
LUCIFERASE ACTIVITY (RLU)

Figure 7

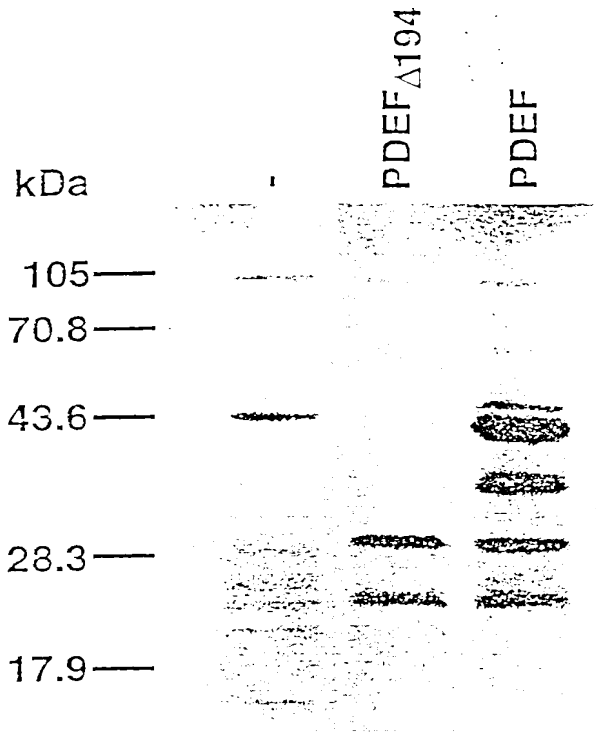


Figure 9

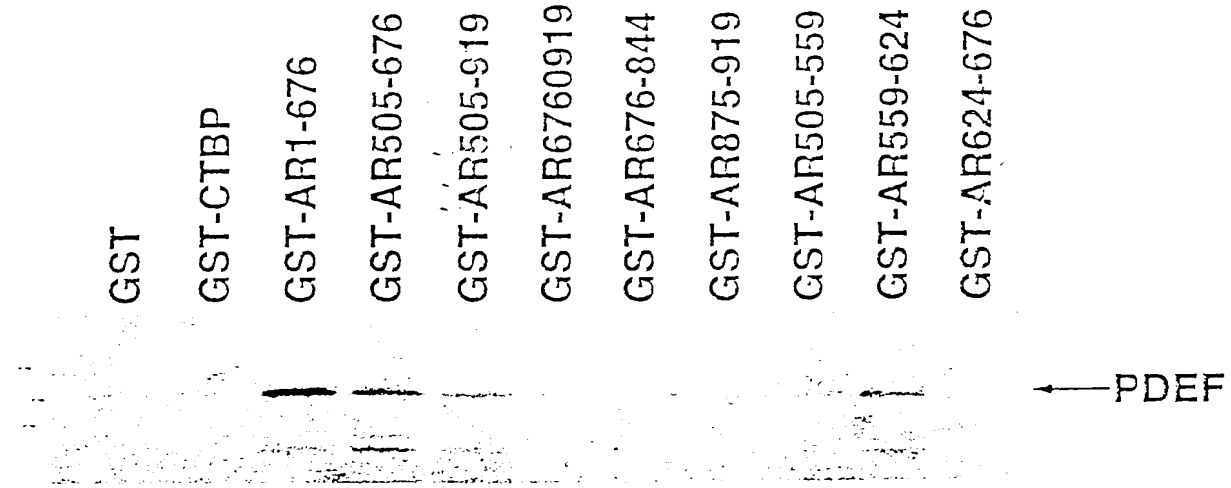


FIGURE 10

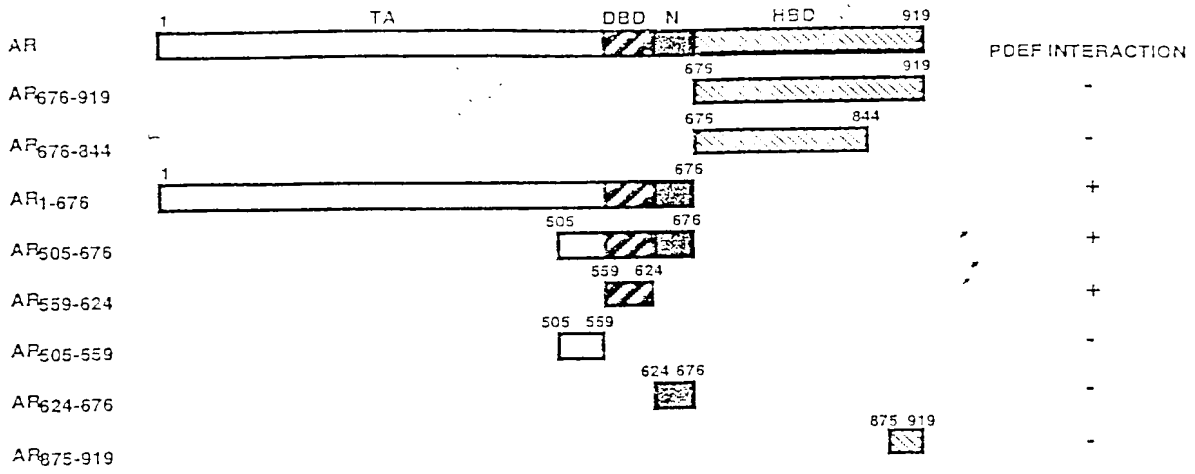


Figure 8

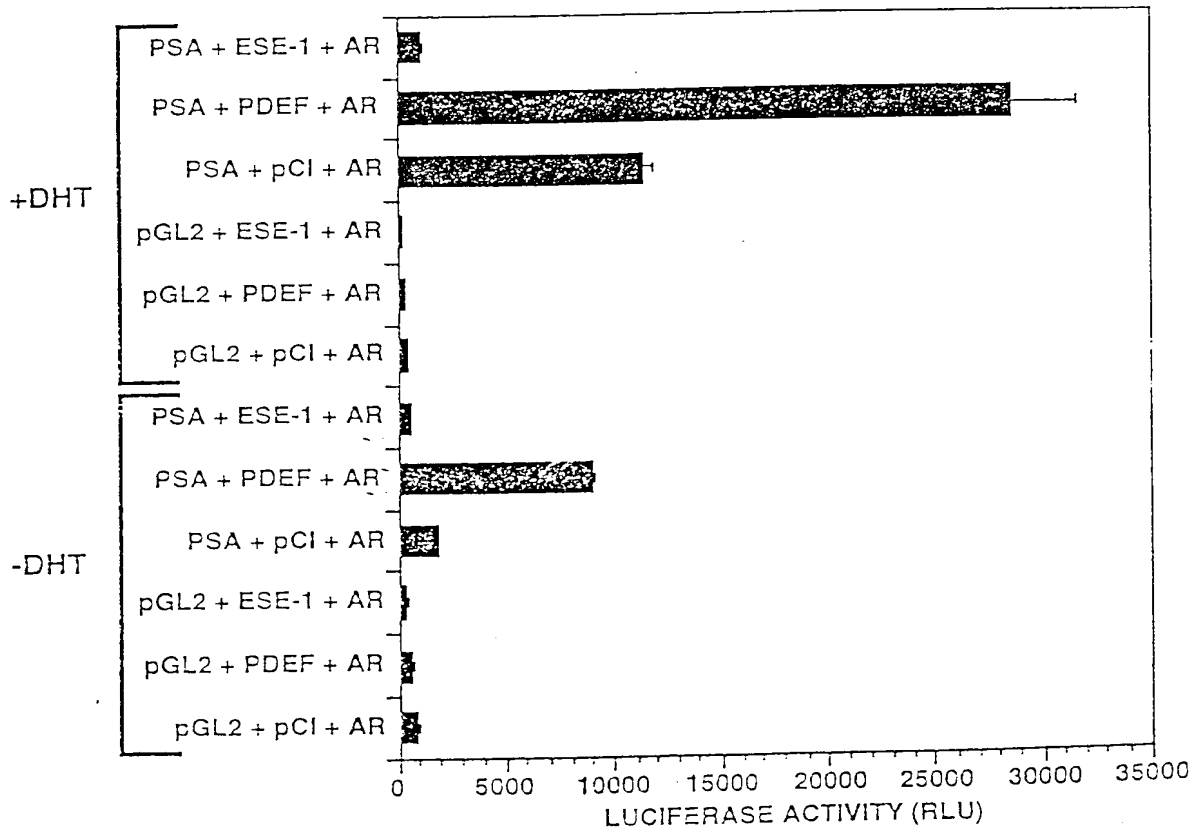


Figure 11